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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/733,507DATE: 12/21/2000  
TIME: 08:41:11Input Set : A:\81601-3.pct.seqlist.txt  
Output Set: N:\CRF3\12212000\I733507.raw

3 <110> APPLICANT: Agriculture and Agri-Food Canada; The University of Saskatchewan  
 5 <120> TITLE OF INVENTION: Cyclin Dependant Kinase Inhibitors as Plant Growth  
 6 Regulators  
 8 <130> FILE REFERENCE: 81601-3  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/733,507  
 C--> 11 <141> CURRENT FILING DATE: 2000-12-02  
 13 <150> PRIOR APPLICATION NUMBER: CA 2,256,121  
 14 <151> PRIOR FILING DATE: 1998-12-31  
 16 <160> NUMBER OF SEQ ID NOS: 16  
 18 <170> SOFTWARE: PatentIn Ver. 2.0  
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 21 <211> LENGTH: 904  
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 44 1  
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 47 Val Arg Lys Tyr Arg Lys Ala Lys Gly Ile Val Glu Ala Gly Val Ser  
 48 5 10 15  
 50 tca acq tat atg caq cta cgg agc cgq aga att gtt tat gtt aga tcg 153  
 51 Ser Thr Tyr Met Gln Leu Arg Ser Arg Arg Ile Val Tyr Val Arg Ser  
 52 20 25 30  
 54 gaa aaa tca agc tct gtc tcc gtc gtc ggt gat aat gga gtt tcg tcg 201  
 55 Glu Lys Ser Ser Ser Val Val Gly Asp Asn Gly Val Ser Ser  
 56 35 40 45  
 58 tct tgt agt gga agc aat gaa tat aag aag aaa gaa tta ala cat ctc 249  
 59 Ser Cys Ser Gly Ser Asn Glu Tyr Lys Iys Lys Glu Leu Ile His Leu  
 60 50 55 60 65  
 62 gag gag gaa gat aaa gat ggt gac act gaa acg tcg acg tat cga cgg 297  
 63 Glu Glu Glu Asp Asp Gly Asp Thr Glu Thr Ser Thr Tyr Arg Arg  
 64 70 75 80  
 66 gtg acg aag agg aag ctc ttt gaa aat ctg aga gag gag gag aag gaa 345  
 67 Val Thr Lys Arg Lys Leu Phe Glu Asn Leu Arg Glu Glu Lys Glu

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71	Glu Leu Ser Lys Ser Met Glu Asn Tyr Ser Ser Glu Phe Glu Ser Ala			
72	100	105	110	
74	gtt aaa gaa tcg tta gat tgt tgt tgc ggg aag aac acg atg gag			441
75	Val Lys Cys Cys Ser Leu Asp Cys Cys Ser Gly Arg Lys Thr Met Glu			
76	115	120	125	
78	gag acg gtg acg gcg qag gag gag aag gca aac ttg atg acg gag			489
79	Glu Thr Val Thr Ala Glu Glu Glu Lys Ala Lys Leu Met Thr Glu			
80	130	135	140	145
82	atg cca acg gaa tcg gaa att gaa gat ttt ttt gtg qaa gct gag aac			537
83	Met Pro Thr Glu Ser Glu Ile Glu Asp Phe Phe Val Glu Ala Glu Lys			
84	150	155	160	
86	caa ctc aaa gaa aaa ttc aag aac tac aat ttc gat ttc gag aag			585
87	Gln Leu Lys Glu Lys Phe Lys Lys Tyr Asn Phe Asp Phe Glu Lys			
88	165	170	175	
90	gag aac cca tta gaa gga cgt tac gaa tgg gta aag tta gag			627
91	Glu Lys Pro Leu Glu Gly Arg Tyr Glu Trp Val Lys Leu Glu			
92	180	185	190	
94	tqaqaqaa qaaqaagttt atgggttttt tttaactttt tttagattta atatttcagg			687
96	qaataaagta attttattttt gtgtatttg aaataataaga tttagtaggag gaatgtttt			747
98	agaagtagca aatttgcacag aaaaagaqa aagcttttta acagattttt qagccccagaa			807
100	aagtcgtgtc ttttagctc acttttaccc ctcttcgaa ttttgcgtat ctttttagcat			867
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120	Ser Ser Cys Ser Gly Ser Asn Glu Tyr Lys Lys Lys Glu Leu Ile His			
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123	Leu Glu Glu Asp Lys Asp Gly Asp Thr Glu Thr Ser Thr Tyr Arg			
124	65	70	75	80
126	Arg Val Thr Lys Arg Lys Leu Phe Glu Asn Leu Arg Glu Glu Lys			
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129	Glu Glu Leu Ser Lys Ser Met Glu Asn Tyr Ser Ser Glu Phe Glu Ser			
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132	Ala Val Lys Glu Ser Leu Asp Cys Cys Ser Gly Arg Lys Thr Met			
133	115	120	125	
135	Glu Glu Thr Val Thr Ala Glu Glu Glu Lys Ala Lys Leu Met Thr			
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138	Glu Met Pro Thr Glu Ser Glu Ile Glu Asp Phe Phe Val Glu Ala Glu			
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226 <400> SEQUENCE: 6  
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 229 qcqagaatt cagcaggcgc qtcqgagacq aqgtttttta taqtacqacq qcqagattct 120  
 231 cctccggtrg aagaacatcg tcaaatrcaa qaagaaggat cgtccggttt qttgttgtct 180  
 233 acatcgaaag agaaatcgua acggagaatc gaatlttgtag atctlgagga aaataacgg 240  
 235 gacgatcgatc aaacagaaac gtcgtggatt tacatgtttt tgaatlaagag tgaggaaatcg 300  
 237 atqaaatcaiqq attccttctt qttgtgttta qaaatqtaq aqtcilcgcq cagglttaaqq 360  
 239 aqagatctcc atqagacggt qaaggaaagct qagtttagaaag acttlttca ggttggcggaq 420  
 241 aaagatcttc ggaataaqtgtt gttgtatgt tctatgtaaat ttaacttcga ttccqaaqaa 480  
 243 gatgagccac tlggllgggg aagatcagc tggtttaaat tgaalccatg aagaagacga 540  
 245 tggatgtttt gatgtatattt gttttttttttttaacaaactt aqgttactt tattttttttt ctgtatataat 600  
 247 ctttgctttt attttttttttaacaaactt caaatqtaq ttttttttttctc tcgaataatc 660  
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 251 ttccctcgatt aataaaactat aagttttaaa ctaaa 755  
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 255 <211> LENGTH: 824  
 256 <212> TYPE: DNA  
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 262 aqgcgagac ttgcgaaqaa aqcttcacgc acaacgtttt caccactgaa gaaaaacqaa 120  
 264 cttaaatgtttt ctctgttttcc atcaccggac tctcatgacq tcatcggtttt cgggttttca 180  
 266 tctttttccg ttgtttcgcc ggcggcttttta ggttctgtat aatgtttttt taccatcggt 240  
 268 ggaqaayaaa gllgatcgatc ctgcgtatc aqctccgggtt gtttccatqaa 300  
 270 qaaatcgcqaa aqaaacatgc tgcgtttttt gtaqatcttq aqgttcatca aatcgaaacc 360  
 272 gaaatccqaa ccttcacattt catccacggc aatttcgaaq aqagacgqg tccatgtgtt 420  
 274 ggggttttgg qaaqaaqccac aacagaaatq gaaatccatc cggccaaacgaa qagaaaaacca 480  
 276 ccgggggttgg qaaqaaqactcc aacqggccgcq gagattqagg atttttttttcc qgagcttagag 540  
 278 aqtcacggatc ataayaagaa qcaatttcata qaaaggataca acttcgatc ttttcaatgac 600  
 280 gaaatccgttgg aqgttcttc aqatggatc cgttccatc ccatcaaaaa gcaatattcca 660  
 282 tccatgtatc aqacaaqaqaa aaaaatggat ttttttttcc ttttttttttccatq 720  
 284 aqgttcttc ttttttttttcc ttttttttttcc ttttttttttccatq 780  
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 299 ttacgttccatc cggcggatc aqgttgcgtt tttttttttt tttttttttt tttttttttt 180  
 301 tcaaggatccatc gtttttttttcc ttttttttttcc ttttttttttcc ttttttttttcc 240  
 303 tcaaggatccatc gtttttttttcc ttttttttttcc ttttttttttcc ttttttttttcc 300  
 305 ttttttttttcc ttttttttttcc ttttttttttcc ttttttttttcc ttttttttttcc 360  
 307 aatccatc ttttttttttcc ttttttttttcc ttttttttttcc ttttttttttcc 420  
 309 ttttttttttcc ttttttttttcc ttttttttttcc ttttttttttcc ttttttttttcc 480  
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Input Set : A:\81601-3.pct.seqlist.txt  
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 328 aacatgttc qttttqaatac aagacacacgc acaaggggaaq gcaacgcctt taaactttgtt 180  
 330 gaggatatqg agatcatgtt tacccaggg tctagcatac qgtcgatgtt cagaccaacc 240  
 332 aaagagtaca caaggaaaca aqataaactg alocggacca clactgaaat ggaggaggatc 300  
 334 tttgcataatg caqagcagca qcaacacayaqq ctattcatgg agaaagtacaa cttcgcacat 360  
 336 qtgaatqata tcccccttcag cggacqttac qaattgggtgc aagtccaaacc atgaaagtctc 420  
 338 aaaggaaaca qctccaaag aacttggatqg aqattagaga attgtatgg agtttaacq 480  
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 346 <213> ORGANISM: Arabidopsis thaliana  
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 352 Ser Ser Thr Tyr Met Cln Leu Arg Ser Arg Arg Ile Val Tyr Val Arg  
 353 20 25 30  
 355 Ser Glu Lys Ser Ser Ser Val Ser Val Val Gly Asp Asn Gly Val Ser  
 356 35 40 45  
 358 Ser Ser Cys Ser Gly Ser Asn Glu Tyr Lys Lys Lys Glu Leu Ile His  
 359 50 55 60  
 361 Leu Glu Glu Glu Asp Lys Asp Gly Asp Thr Glu Thr Ser Thr Tyr Arg  
 362 65 70 75 80  
 364 Arg Gly Thr Lys Arg Lys Leu Cys Glu Asn Leu Arg Glu Glu Glu Lys  
 365 85 90 95  
 367 Glu Glu Leu Ser Lys Ser Met Glu Asn Tyr Ser Ser Glu Phe Glu Ser  
 368 100 105 110  
 370 Ala Val Lys Glu Ser Leu Asp Cys Cys Cys Ser Gly Arg Lys Thr Met  
 371 115 120 125  
 373 Glu Glu Thr Val Thr Ala Glu Glu Glu Lys Ala Lys Leu Met Thr  
 374 130 135 140  
 376 Glu Met Pro Thr Glu Ser Glu Ile Glu Asp Phe Phe Val Glu Ala Glu  
 377 145 150 155 160  
 379 Lys Glu Leu Lys Glu Lys Phe Lys Lys Lys Tyr Asn Phe Asp Phe Glu  
 380 165 170 175  
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 388 <212> TYPE: PRT  
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VERIFICATION SUMMARY DATE: 12/21/2000  
PATENT APPLICATION: US/09/733,507 TIME: 08:41:32

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date